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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

April 27, 2003, 08:52:11; Search time 28 Seconds (without alignments) 710.708 Million cell updates/sec Run on:

US-09-836-960-5 1097 1 MYSAPSACTCLCLHFLLLCF......PFKYTTVTKRSRRIRPTHPA 207 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 seqs, 96134422 residues Searched:

283224

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Description	ilibroblast growth fibroblast growth fibroblast growth keratinocyte growth keratinocyte growth keratinocyte growth fibroblast growth protein let-756 [i fibroblast growth acidic fibroblast growth f	dacture introplast basic fibroblast g fibroblast growth embryonic fibrobla basic fibroblast g basic fibroblast g
SUMMARIES	GG2292 A46245 A46245 A36301 A36301 148610 S26649 S26649 A6137 S04147 S04147 S04147 A913560 A60721 A60721 A60721 A60721 A60721 A60721 A60721	GKBOA JGS940 S23595 S00185 GKBOB
DB	200100000000000000000000000000000000000	100011
Length	2115 2115 2116 2116 2116 2116 2117 2117 2117 2117	189 189 207 187 146
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a Query Match	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	111111
Score	1000 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	159.5 159.5 159.5 157.5
Result No.	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	224 224 238 238 238

fibroblast growth	fibroblast growth	fibroblast growth	acidic fibroblast	fibroblast growth	transforming prote	basic fibroblast g	basic fibroblast g	fibroblast growth	fibroblast growth	fibroblast growth	basic fibroblast g	fibroblast growth	fibroblast growth	basic fibroblast g
S20102	TVMSHS	JC5941	A60130	I50588	S39582	A31674	C37360	A36207	JC4268	S68144	A32398	S14192	146711	\$31622
77	٦, ١	~	7	~	Н	~	~	7	7	~	7	7	~	7
208	202	207	155	220	237	154	154	264	206	266	210	208	137	164
14.3	14.3	14.3	14.1	14.0	14.0	13.8	13.8	13.8	13.5	13.4	13.4	13.3	13.2	13.2
157	156.5	156.5	154.5	154	154	151.5	151.5	151	148.5	147.5	146.5	146	144.5	144.5
30	32	33	34	32.	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

 RESULT 1
 GOLOUS fibroblast growth factor 8 precursor - human N;Alternate names: androgen-induced growth factor N;Contains: fibroblast growth factor 8, splice form A
 C;Species: Homo sapiens (man) C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 31-Mar-2000 C;Accession: G02092; S65653; G02394.
 Submitted to the EMBL Data Library, September 1995 A;Reference number: H00790 A;Acression: 607002
 A; Actus: translated from GB/EMBL/DDBJ A; Molecule type: mRNA
 A; Vestoues: L-11> CALS CALL: U36223; NID: 91143261; PID: 91143262 R; Tanaka, A:, Miyamoto, K:, Matsuo, H:; Matsumoto, K:; Yoshida, H:
 A.Title: Human androgen-induced growth factor in prostate and breast cancer cells: in A;Reference number: 865653; MUID:95255551; PMID:7737407
A;Accession: S65653 A;Status: preliminary A;Molecule type: DMs; mRNA
A,residues: 1-110 view. A,cross-references: EMBL:S78465; EMBL:S78466; NID:g999171; PID:g999172; GB:D38752; N R;ROY-Burman, P.
submitted to the EMBL Data Library, January 1996 A;Reference number: H01168
A:Molecule type: mRNA
A;Residues: 1-23,35-215 <roy> A;Residues: BMBL:U46211; NID:g1184864; PID:g1184865 C:Genetics: EMBL:U46211; NID:g1184864; PID:g1184865</roy>
 A;Gene: GDB:FGFB; AIGF A;Cross-references: GDB:591889; OMIM:600483 A;Map position: 10q25-10q26 C;Keywords: alternative splicing: blocked amino end; pyroglutamic acid
F;1ZJVomdan: signal sequence #status predicted <2LZJVomdan: signal sequence #status predicted <mat> F;23.215/Product: fibroblast growth factor 8 #status predicted <mat> F;23,35-215/Product: fibroblast growth factor 8. splice form A #status predicted <mat #status="" (gln)="" (in="" acid="" carboxylic="" f;23="" form)="" mature="" modified="" predi<="" pyrrolidone="" site:="" td=""></mat></mat></mat>
Query Match 53.9%; Score 591; DB 2; Length 215; Best Local Similarity 57.3%; Pred. No. 6.3e-45; Matches 110; Conservative 35; Mismatches 45; Indels 2; Gaps 2;
 QY 1 MYSAPSACTCI.CLHFILI.CFQVQVLVABENVDFRIHVENQTRARDDVSRKQLRI.YQLYSR 60

61 TSGKHIQVL-GRRISARGEDGDKYAQLLVETDTFGSQVRIKGKETEFYLCMNRKGKLVGK 119

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A; Accession: A36301
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Matches
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NiAlternate names: androgen-induced growth factor
C;Species: Mus musculus (house mouse)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 17-Mar-2000
C;Accession: A66245; 169194; SS3114
R;Tanaka, A.; Miyamoto, K.; Minamino, N.; Takeda, M.; Sato, B.; Matsuo, H.; Matsumoto, R
Proc. Natl. Acad. Sci. U.S.A. 89, 8928-8932, 1992
A;Title: Cloning and characterization of an androgen-induced growth factor essential for A;Reference number: A46245; MUID:93028380; PMID:1409588
A;Accession: A46245
A;Accession: Preliminary
A;Molecnia + .... - ....
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A;Molecule type: mRNA
A;Cross-references: EMBL:U18673; NID:g619919; PIDN:AAA65387.1; PID:g619920
B;Mahmood, R.; Bresnick, J.; Hornbruch, A.; Mahony, C.; Morton, N.; Colquhoun, K.; Marti
B;Molecule to the EMBL Data Library, March 1995
A;Description: FGF-8 in the mouse embryo: a role in the initiation and maintenance of 11
A;Reference number: S53114
A;Accession: S53114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Experimental source: mammary carcinoma, clone pSC17
A:Note: sequence extracted from NCBI backbone (NCBIN:115358, NCBIP:115360)
A:Note: sequence extracted from NCBI backbone (NCBIN:115358, NCBIP:115360)
B:MacArthur, C.A.; Shankfar, D.B.; Shackleford, G.M.
J. Virol. 69, 2501-2507, 1995
A:Title: Fgf-8, activated by proviral insertion, cooperates with the Wnt-1 transgene in A:Reference number: 149194; MUID:95191029; PMID:7884899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA; protein
A;Residues: 1-215 <TAN>
A;Cross-references: GB:D12482; NID:g220324; PIDN:BAA02050.1; PID:d1002532; PID:g220325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5,
A;Residues: 1-23,35-215 <WAH>.
A;Cross-references: EMBL:Z48746; NID:g732820; PIDN:CAA88637.1; PID:g732821 C;Genetics: A;Gene: Fgf-8 C;Keywords: alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 TSGKHIQVL-GRRISARGEDGDKYAQLLVETDTFGSQVRIKGKETEFYLCMNRKGKLVGK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59
                                                                          120 PDGTSKECVFIEKVLENNYTALMSAKYSGWYVGFTKKGRPRKGPKTRENQODVHFMKRYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 PDGTSKECVFIEKVLENNYTALMSAKYSGWYVGFTKKGRPRKGPKTRENQQDVHFMKRYP
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                                                                                                                                                                             180 KGQPELQKPFKY 191
                                                                                                                                                                                                                            RGHHTTEQSLRF 191
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A; Residues: 1-23,35-215
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Cibroblast growth factor-17 - rat
Cispecies: Rattus norvegicus (Norway rat)
Cispecies: Rattus norvegicus (Norway rat)
Cispecies: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
Ciscossion: JG5972
Riboshikawa, M.; Ohbayashi, N.; Yonamine, A.; Konishi, M.; Ozaki, K.; Fukui, S.; Itoh Biochem. Biophys. Res. Commun. 244, 187-191, 1998
A:Title: Structure and expression of a novel fibroblast growth factor, FGF-17, preference number: JC5972; MuID:98183421; PMID:9514906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-194 <FIN>
A; Residues: 1-194 <FIN>
A; Cross-references: GB:M60828; NID:g186738; PIDN:AAA63210.1; PID:g186739; GB:M25295
A; Cross-references: GB:M60828; NID:g186738; PIDN:AAA63210.1; PID:g186739; GB:M25295
B; Rubin, J.S.; Osada, H.; Finch, P.W.; Taylor, W.G.; Rudlkoff, S.; Aaronson, S.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 802-806, 1989
A; Reference number: A31453; MUID:89128865; PMID:2915979
A; Reference number: A31453; MUID:89128865; PMID:2915979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title: Human KGF is FGF-related with properties of a paracrine effector of epitheli A; Reference number: A36301; MUID:89368897; PMID:2475908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A. Molecule type: protein
A. Residues: 'X' 33-44 <RUB>
A. Experimental source: embryonic lung cell fibroblast line M426
A. Experimental source: embryonic lung cell fibroblast line M426
R. Kelley, M.J.; Pech, M.J. Seuanez, H.N.; Rubin, J.S.; O'Brien, S.J.; Aaronson, S.A. Proc. Natl. Acad. Sci. U.S.A. 89, 9287-9291, 1992
A.Title: Emergence of the keratinocyte growth factor multigene family during the grean Keference number: A46289; MUID:93028449; PMID:1409637
A. Accession: A46289.
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R; Aaronson, S.A.; Bottaro, D.P.; Miki, T.; Ron, D.; Finch, P.W.; Fleming, T.P.; Ahn, Ann. N. Y. Acad. Sci. 638, 62-77, 1991
A; Title: Keratinocyte growth factor. A fibroblast growth factor family member with un A; Reference number: 151958; MUID:92152720; PMID:1664700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 LCLHFLLLCFQVQVLVAEEN---VDFRIHVENQTRARDDVSRKQLRLYQLYSRTSGKHIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 566; DB 2; LP Pred. No. 1e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               51.6%; Scc. No. 1c
54.4%; Pred. No. 1c
... 37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 -PELOKPFKY----TTVTKRSRR 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | || |:: | || |:| | HAERQKQFEFVGSAPTRRTKRTRR 211
                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: GB: AB009250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 54.4 ses 111; Conservative
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A; Residues: 97-194 <KEL>
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A;Molecule type: mRNA
A;Residues: 1-216 <HOS>
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during mouse development sugg

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Indels

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fibroblast growth factor 7 precursor - rat
N.Alternate names: keratinocyte growth factor
C.Species: Rattus norvegicus (Norway rat)
C.Species: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 16-Jul-1999
C.Accession: $26049; $78446
R.Yan, G.; Nikolaropoulos, S.; Wang, F.; McKeehan, W.L.
In Vitro Cell. Dev. Biol. 27, 437-438, 1991
A.Fille: Sequence of rat keratinocyte growth factor
A.Reference number: $26049
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999 C;Accession: 148610; S33227 R;Mason, I.J.; Fuller-Pace, F.; Smith, R.; Dickson, C. Ms.C. Jo., Fuller-Pace, F.; Smith, R.; Dickson, C. A;Tille: FGF-7 (keratinocyte growth factor) expression during mouse developm A;Atille: FGF-7 (keratinocyte growth factor) expression during mouse developm A;Accession: 148610 MUID:94242659; PMID:8186145 A;Accession: 148610 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-194 ARBS. A;Residues: 1-194 ARBS. A;Accession: EMBL:222703; NID:9297755; PIDN:CAA80403.1; PID:9297756 C;Superfamily: fibroblast growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Reference number: S78446
A, Accession: S78446
A, Accession: S78446
A, Molecule type: mRNA
A, Residues: 1-16, P', 18-100, 'M', 102-123, 'O', 125-150, 'S', 152-194 < YAW>
A, Residues: 1-16, 'P', 18-100, 'M', 102-123, 'O', 125-150, 'S', 152-194 < YAW>
A, Cross-references: EMBL: X56551; NID: 956707; PIDN: CAA39892.1; PID: 956708
C; Superfamily: fibroblast growth factor: heparin binding; mitogen C; Reywords: extracellular protein; growth factor; heparin binding; mitogen C; Reywords: signal sequence #status predicted < SIG>
F; 32-194/Product: fibroblast growth factor 7 #status predicted < MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | ||: |: :|: || || 50 ERHITSYDYMEGGDIRVRRLFCRTQWY-----LRIDKRGKVKGTQEMKNSYNIMEIRTV 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92 TFGSQVRIKGKETEFYLCMNRKGKLVGKPDGTSKECVFIEKVLENNYTALMSAK--YSG- 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104 AVGI-VAIKGVESEYYLAMNKEGKLYAKKE-CNEDCNFKELILENHYNTYASAKWTHSGG 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50 ERHTRSYDYMEGGDIRVRRLFCRTQWY-----LRIDKRGKVKGTQEMRNSYNIMEIRTV 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38 ENQTRARDDVSRKQLRLYQLYSRTSGKHIQVLGRRISARG-----EDGDKYAQLLVETD
                                                                                                                                                                                                                                                                                                                                                                                       Length 194;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    51;
                                                                                                                                                                                                                                                                                                                                                                                       Query Match 17.6%; Score 193; DB 2; Best Local Similarity 35.8%; Pred. No. 8.7e-10; Matches 53; Conservative 26; Mismatches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17.3%; Score 190; DB 2; 35.1%; Pred. No. 1.6e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A)Accession: S26049
A;Molecule type: mRNA
A;Residues: 1-194 <YAN>
A;Crooss-references: EMBL:X56551
B;Yan, G.
submitted to the EMBL Data Library, February 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149 -WYVGFTKKGRPRKGPKTRENQQDVHFM 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149 -WYVGFTKKGRPRKGPKTRENQQDVHFM 175
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Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                             A) Note: the human genome contains about 16, intron-containing, partial copies of this C; Superfamily: fibroblast growth factor C; Superfamily: fibroblast growth factor; heparin binding; mitogen C; Keywords: extracellular protein; growth factor; heparin binding; mitogen F; 1-31/Domain: signal sequence #status predicted <51G>
F; 32-194/Product: fibroblast growth factor 7 #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7;
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8
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Cispecies: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
Cispecies: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
Cispecies: Orieb-1995 #sequence_revision 20.Feb-1995 #text_change 16-Jul-1999
Cistocession: 549501
RMitchell, J.E.A.; McInnes, C.J.
Submitted to the EMBL Data Library, October 1994
A:Description: Cloning of a cDNA encoding ovine keratinocyte growth factor.
A:Reference number: 549501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA AREsidues: 1-194 <MIT>
A;Residues: 1-194 <MIT>
A;Cross-references: EMBL:Z46236; NID:g559503; PIDN:CAA86306.1; PID:g559504 C;Superfamily: fibroblast growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 IQVLGRRISARG-----EDGDKYAQLLVETDTFGSQVRIKGKETEFYLCMNRKGKLVGK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PDGTSKECVFIEKVLENNYTALMSAKYS----GWYVGFTKKGRPRKGPKTRENQQDVHFM 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 SRTSGKHIQVLGRRISARG-----EDGDKYAQLLVETDTFGSQVRIKGKETEFYLCMNR 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 CRTQWY-----LRIDKRGKVKGTQEMKNNYNIMEIRTVAVGI-VAIKGVESEYYLAMNK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 KGKLVGKPDGTSKECVFIEKVLENNYTALMSAK--YSG--WYVGFTKKGRPRKGPKTREN 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 CFHIICLVGTISLACNDMTPEQMATNVNCSSPERHTRSYDYMEGGDIRVRRLFCRTQWY- 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 CLHFLLLCFQVQVL---VAEENVDFRIHV---ENQTRARDDVSRKQLRLYQLYSRTSGKH 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 PSACTCLCLHFLLLCFQVQVL---VAEENVDFRIHV---ENQTRARDDVSRKQLRLYQLY 58
                           A; Molecule type: mRNA
A; Residues: 1-194 <AAR>
A; Cross-references: GB:S81661; NID:g245438; PIDN:AAB21431.1; PID:g245439
C; Genetics: GB:RGF7
A; Gene: GBB:RGF7
A; Cross-references: GDB:131444; OMIM:148180
A; Map position: 15q13-15q22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24;
                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 30.6%; Pred. No. 7.1e-10;
Matches 55; Conservative 34; Mismatches 67; Indels ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 193; DB 2; Length 194;
Pred. No. 8.7e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72; Indels
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keratinocyte growth factor Fgf-7 - mouse
C;Species: Mus musculus (house mouse)
   A;Status: translated from GB/EMBL/DDBJ
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Best Local Similarity 31.09
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QKTAHFL 189
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154
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S66486
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                Tibroblast somatotropin-20 - African clawed frog
N;Alternate names: fibroblast growth factor-20
C;Species: Xenopus laevis (African clawed frog)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C;Accession: JG7082
R;Koga, C.; Adati, N.; Nakata, K.; Mikoshiba, K.; Furuhata, Y.; Sato, S.; Tei, H.; Sakak Biochem. Blophys. Res. Commun. 261, 756-765, 1999
A;Title: Characterization of a novel member of the FGF family, XFGF-20, in Xenopus laevi
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A;Residues: 1-208 <KOG>
A;Cross-references: DDBJ:AB012615; NID:95762261; PIDN:BAA83474.1; PID:95762262
C;Superfamily: fibroblast growth factor
C;Keywords: differentiation; fibroblast; growth factor; heparin binding
                                                                                                                                                                                                                                                                                                                                                138 YTALMSAKY----KRYPKGRPRKGPKTRENQQDVHFM-----KRYPKG-- 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDKYAQLLVE-TDTFGSQVRIKGKETEFYLCMNRKGKLVGKPDGT-SKECVFIEKVLENN 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 KGKETEFYLCMNRKGKLVGKPDGTSKECVFIEKVLENNYTALMSAKY----SG--WYVGF 153
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                                                                                                                                                                                                                                                                                                           62;
                                                                                                                                                                                                                                                                                  Length 413;
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                                                                                                                                                                                                                                                                                                        62;
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                                                                                                                                                                                                                                                                              ; Score 190; DB 2;
; Pred. No. 3.9e-09;
31; Mismatches 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.5%; Score 181; DB 2;
37.2%; Pred. No. 1.1e-08;
tive 21; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------QPELQKPFKYTTVTKRSRRIRPTHP 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    226 VTDLVVASLFHQPPSHPLFRQQTVTK-----PPNP 255
                                                                                                                                                                                                                                                                             17.3%; 28.2%;
                                                                                                                                                                                                                                                                                                        61; Conservative
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Best Local Simi
Matches 58;
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Matches 6
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fibroblast growth factor 4 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C;Accession: S78506; S50858; I50710
R;Niswander, L.
Submitted to the EMBL Data Library, September 1994
A;Reference number: S78506
A;Molecule type: DNA
A;Residues: 1-194 <NIS>
A;Residues: 1-194 <NIS
A;Resid
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C.Species: Mas musculus (house mouse)
C.Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C.Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C.Accession: S66486
A.Stetus: 370, 231-235, 1995
A.Title: Retinoic acid induces gene expression of fibroblast growth factor-9 during in A.Recession: S66486
A.Accession: S66486
A.Status: preliminary
A.Moccession: S66486
A.Status: preliminary
A.Moccession: 1-208 A.SEO>
A.Coss.references: EMBL:D38258; NID:g1107458; PIDN:BAA07410.1; PID:g1107459
C.Superfamily: fibroblast growth factor
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A; Residues: 1.136, '0', 137-194, '1' <NIW>
A; Cross-references: EMBL:U14654; NID:g609347; PIDN:AAA58706.1; PID:g609348
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LRLYQLYSRTSGKHIQVL-GRRISARGEDGDKYAQLLVETDTFGSQVRIKGKETEFYLCM 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 15.7%; Score 172; DB 2; Length 19
Local Similarity 36.5%; Pred. No. 6.3e-08;
nes 54; Conservative 16; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 15.7%; Score 172; DB 2; Best Local Similarity 35.2%; Pred. No. 6.8e-08; Matches 51; Conservative 22; Mismatches 60
                                                            TKKGRPRKGPKTRENQQDVHFMKR--YPKGQPELQK 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: fibroblast growth factor
C;Keywords: growth factor; transforming protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     150 YVGFTKKGRPRKGPKTRENQQDVHFMKR 177
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Alternate names: arGF; rGF-1
C; Species: Mus musculus (house mouse)
C; Accession: D37360; JG5231
B; Hebert, J.M.; Basilico, C; Goldfarb, M.; Haub, O.; Martin, G.R.
B; Hebert, J.M.; Basilico, C; Goldfarb, M.; Haub, O.; Martin, G.R.
B; Reference number: A37360; MUD:90201563; PMID:2318343
A; Reference number: A37360; MUD:90201563; PMID:2318343
A; Residues: 1-155 < HEBS
A; Cross-references: GB:M30641; NID:9193284; PIDN:AAA37618.1; PID:9309236
B; Madiai, F.; Hackshaw, K.V.; Chlu, I.M.
A; Reference number: JG5231
A; Title: Cloning and characterization of the mouse Fgf-1 gene.
A; Reference number: JG5231
A; Accession: JG5231
A; Accession: JG5231
A; Reference number: JG5231
A; Residues: 1-155 < AAD>
A; Cross-references: GB:U36456
C; Comment: This protein is an inducer of neovascularization in angiogenic disease inc.
C; Genetics:
C; Genetics: Fgf-1, G1/2
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(ibroblast growth factor 4 - human

(ibroblast growth factor 4 - human

(ibroblast growth factor 5 - human

(ibroblast growth factor 6 - human

(ibroblast growth factor 6 - human

(ibroblast growth 6 - hu
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                                       LYSRTSGKHIQVL-GRRISARGEDGDKYAQLLVETDTFGSQVRIKGKETEFYLCMNRKGK 115
                                                                                                                                                                                                                LVGKPDGTSKECVFIEKVLENNYTALMSAKYS--GWYVGFTKKGRPRKGPKTRENQQDVH 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57 LYSRTSGKHIQVL-GRRISARGEDGDKYAQLLVETDTFGSQVRIKGKETEFYLCMNRKGK 115
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                                                                           Gaps
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Pred. No. 5.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.6%; Scor.
32.0%; Pred. No. 5...
'''A 29; Mismatches
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C,Superfamily: fibroblast growth factor
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les 39; Conserva
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FL 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FL 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 39
                                       21
                                                                                                                                                                                                                                                                                                                                                                                             147
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Mol. Cell. Biol. 13, 4251-4259, 1993
A;Title: Molecular cloning of a novel cytokine cDNA encoding the ninth member of the
A;Reference number: 448137; MUID:93309459; PMID:8321227
A;Status: preliminary
A;Molecule type: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alternate names: heparin-binding growth factor 1
C.Species: Rattus norvegicus (Norway rat)
C.Species: Rattus norvegicus (Norway rat)
C.Species: Rattus norvegicus (Norway rat)
C.Species: 188-1990 #sequence_revision 28 Feb-1990 #text_change 16-Jul-1999
C.Specession: S04147
R.Goodrich, S.P.; Yan, G.C.; Bahrenburg, K.; Mansson, P.E.
Nucleic Acids Res. 17, 2867, 1989
A.Title: The nucleotide sequence of rat heparin binding growth factor 1 (HBGF-1).
A.Feference number: S04147; MUID:89240051; PMID:2470029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                fibroblast growth factor 9 - human N:Alternate names: glia-activating factor C:Species: Homo sapiens (man) C:Species: 1-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
61 LRRRQLYCRT-GFHLEIFPNGTIQGTRKDHSRFGILEFISIAVG-LVSIRGVDSGLYLGM 118
                                                                                                        A; Cross-references: GB:D14838; NID:9391718; PIDN:BAA03572.1; PID:9391719
A; Experimental source: foreskin
A; Note: sequence extracted from NCBI backbone (NCBIN:134640, NCBIP:134641)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 NRKGKLVGKPDGTSKECVFIEKVLENNYTALMSAKYS-----GWYVGFTKKGRPRKGPK 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 LRLYQLYSRTSGKHIQVL-GRRISARGEDGDKYAQLLVETDTFGSQVRIKGKETEFYLCM 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 NRKGKLVGKPDGTSKECVFIEKVLENNYTALMSAKYS-----GWYVGFTKKGRPRKGPK 164
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A; Residues: 1-155 < GOO>
A; Cross-references: EMBL:X14232; NID:956351; PIDN:CAA32448.1; PID:956352
C; Superfamily: flbroblast growth factor
C; Keywords: growth factor; heparin binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GDB:207221; OMIM:600921
                                                                                                                                                                                                                                                    A; Map position: 13q11-13q12
C; Superfamily: fibroblast growth factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165 TRENOQDVHFMKR--YPKGQPELQK 187
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Best Local Similarity 32.0%
Matches 39; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: A48137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: S04147
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Matches
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us-09-836-960-5.rpr

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A.Molecule type: mRNA
A.Residues: 1-206 <BOV>
A.Residues: 1-206 <BOV>
A.A.Cross-references: GB.MJ7446; NID:g186785; PIDN:AAA59473.1; PID:g307092
G.Comment: This protein is an oncogene for Kaposi's sarcoma. It is homologous to the mou G.Genetics:
A.Gene: GDB:FGF4; HSTF1
A.Gross-references: GB120066; OMIM:164980
A.Map position: 11q13.3-11q13.3
A.Introns: 114/1; 148/3
G.Superfamily: fibroblast growth factor
C.Keywords: growth factor
C.Keywords: growth factor
                                                                                                A;Cross-references: DDBJ:J02986; NID:g184430; PIDN:AABS9555.1; PID:g386788
R;Talra, M.; Yoshida, T.; Miyagawa, K.; Sakamoto, H.; Terada, M.; Sugimura, T.
Proc. Natl. Acad. Sci. U.S.A. 84, 2980-2984, 1987
A;Title: CDNA sequence of human transforming gene hst and identification of the coding A;Reference number: A29876; MUID:87204251; PMID:2953031
A;Accession: A29876
                                                                                                                                                                                                                                                                                                                                                       A)Cross-references: GB:J02986; GB:M16338; NID:g184430; PIDN:AAB59555.1; PID:g386788
R:Delli Bovi, P.; Curatola, A.M.; Kern, F.G.; Greco, A.; Ittmann, M.; Basilico, C.
Gell 50, 729-737, 1987
A;Title: An oncogene isolated by transfection of Kaposi's sarcoma DNA encodes a growth A;Reference number: A29649; MUID:87301716; PMID:2957062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 CMNRKGKLVGKPDGTSKECVFIEKVLENNYTALMSAKYSGWYVGFTKKGRPRKGPKTREN 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
15.5%; Score 170.5; DB 1; Length 206;
Best Local Similarity 36.4%; Pred. No. 9.2e-08;
Matches 47; Conservative 17; Mismatches 56; Indels 9
                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-206 <TAI>
A; Accession: A28417
A; Molecule type: DNA
A; Residues: 1-206 <YOS>
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